

Raw Sequence Listing

Patent Application US/07/625,668A

Group 1814

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: WALLACH, DAVID

NOPHAR, YARON

KEMPER, OLIVER

ENGELMANN, HARTMUT

BRAKEBUSCH, CORD

ADERKA, DAN

(ii) TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
NECROSIS FACTOR BINDING PROTEIN I (TBP-I)

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Browdy and Neimark

(B) STREET: 419 Seventh Street, N.W., Suite 300

(C) CITY: Washington

(D) STATE: DC

(E) COUNTRY: USA

(F) ZIP: 20004

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/625668

(B) FILING DATE: 13-DEC-1990

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: BROWDY, ROGER L

(B) REGISTRATION NUMBER: 25,618

(C) REFERENCE/DOCKET NUMBER: WALLACH4

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-628-5197

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(C) TELEX: 248633

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2175 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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54 (D) TOPOLOGY: linear
55
56 (ii) MOLECULE TYPE: cDNA
57
58
59 (ix) FEATURE:
60 (A) NAME/KEY: CDS
61 (B) LOCATION: 256..1620
62
63 (ix) FEATURE:
64 (A) NAME/KEY: mat_peptide
65 (B) LOCATION: 319..1620
66
67
68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
69
70 CGGCCCAGTG ATCTTGAACC CCAAAGGCCA GAACTGGAGC CTCAGTCCAG AGAATTCTGA 60
71
72 GAAAATTAAA GCAGAGAGGA GGGGAGAGAT CACTGGGACC AGGCCGTGAT CTCTATGCCC 120
73
74 GAGTCTCAAC CCTCAACTGT CACCCCAAGG CACTTGGGAC GTCCTGGACA GACCGAGTCC 180
75
76 CGGGAAGCCC CAGCACTGCC GCTGCCACAC TGCCCTGAGC CCAAATGGGG GAGTGAGAGG 240
77
78 CCATAGCTGT CTGGC ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCG 291
79 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro
80 -21 -20 -15 -10
81
82 CTG GTG CTC CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT 339
83 Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile
84 -5 1 5
85
86 GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT 387
87 Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys
88 10 15 20
89
90 CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC 435
91 Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
92 25 30 35
93
94 AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG GGG 483
95 Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly
96 40 45 50 55
97
98 CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC GCT TCA 531
99 Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser
100 60 65 70
101
102 GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC CGA AAG GAA 579
103 Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu
104 75 80 85
105
106 ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC CGG GAC ACC GTG 627

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107	Met	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp	Arg	Asp	Thr	Val	
108			90					95					100				
109																	
110	TGT	GGC	TGC	AGG	AAG	AAC	CAG	TAC	CGG	CAT	TAT	TGG	AGT	GAA	AAC	CTT	675
111	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	
112		105					110					115					
113																	
114	TTC	CAG	TGC	TTC	AAT	TGC	AGC	CTC	TGC	CTC	AAT	GGG	ACC	GTG	CAC	CTC	723
115	Phe	Gln	Cys	Phe	Asn	Cys	Ser	Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu	
116	120					125					130					135	
117																	
118	TCC	TGC	CAG	GAG	AAA	CAG	AAC	ACC	GTG	TGC	ACC	TGC	CAT	GCA	GGT	TTC	771
119	Ser	Cys	Gln	Glu	Lys	Gln	Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe	
120					140					145					150		
121																	
122	TTT	CTA	AGA	GAA	AAC	GAG	TGT	GTC	TCC	TGT	AGT	AAC	TGT	AAG	AAA	AGC	819
123	Phe	Leu	Arg	Glu	Asn	Glu	Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	
124				155					160					165			
125																	
126	CTG	GAG	TGC	ACG	AAG	TTG	TGC	CTA	CCC	CAG	ATT	GAG	AAT	GTT	AAG	GGC	867
127	Leu	Glu	Cys	Thr	Lys	Leu	Cys	Leu	Pro	Gln	Ile	Glu	Asn	Val	Lys	Gly	
128			170					175					180				
129																	
130	ACT	GAG	GAC	TCA	GGC	ACC	ACA	GTG	CTG	TTG	CCC	CTG	GTC	ATT	TTC	TTT	915
131	Thr	Glu	Asp	Ser	Gly	Thr	Thr	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Phe	
132		185					190					195					
133																	
134	GGT	CTT	TGC	CTT	TTA	TCC	CTC	CTC	TTC	ATT	GGT	TTA	ATG	TAT	CGC	TAC	963
135	Gly	Leu	Cys	Leu	Leu	Ser	Leu	Leu	Phe	Ile	Gly	Leu	Met	Tyr	Arg	Tyr	
136	200					205					210					215	
137																	
138	CAA	CGG	TGG	AAG	TCC	AAG	CTC	TAC	TCC	ATT	GTT	TGT	GGG	AAA	TCG	ACA	1011
139	Gln	Arg	Trp	Lys	Ser	Lys	Leu	Tyr	Ser	Ile	Val	Cys	Gly	Lys	Ser	Thr	
140				220						225					230		
141																	
142	CCT	GAA	AAA	GAG	GGG	GAG	CTT	GAA	GGA	ACT	ACT	ACT	AAG	CCC	CTG	GCC	1059
143	Pro	Glu	Lys	Glu	Gly	Glu	Leu	Glu	Gly	Thr	Thr	Thr	Lys	Pro	Leu	Ala	
144			235						240					245			
145																	
146	CCA	AAC	CCA	AGC	TTC	AGT	CCC	ACT	CCA	GGC	TTC	ACC	CCC	ACC	CTG	GGC	1107
147	Pro	Asn	Pro	Ser	Phe	Ser	Pro	Thr	Pro	Gly	Phe	Thr	Pro	Thr	Leu	Gly	
148			250					255					260				
149																	
150	TTC	AGT	CCC	GTG	CCC	AGT	TCC	ACC	TTC	ACC	TCC	AGC	TCC	ACC	TAT	ACC	1155
151	Phe	Ser	Pro	Val	Pro	Ser	Ser	Thr	Phe	Thr	Ser	Ser	Ser	Thr	Tyr	Thr	
152		265					270					275					
153																	
154	CCC	GGT	GAC	TGT	CCC	AAC	TTT	GCG	GCT	CCC	CGC	AGA	GAG	GTG	GCA	CCA	1203
155	Pro	Gly	Asp	Cys	Pro	Asn	Phe	Ala	Ala	Pro	Arg	Arg	Glu	Val	Ala	Pro	
156	280					285					290					295	
157																	
158	CCC	TAT	CAG	GGG	GCT	GAC	CCC	ATC	CTT	GCG	ACA	GCC	CTC	GCC	TCC	GAC	1251
159	Pro	Tyr	Gln	Gly	Ala	Asp	Pro	Ile	Leu	Ala	Thr	Ala	Leu	Ala	Ser	Asp	

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	300	305	310	
160				
161				
162	CCC ATC CCC AAC CCC CTT CAG AAG TGG GAG GAC AGC GCC CAC AAG CCA			1299
163	Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro			
164	315	320	325	
165				
166	CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC GCC GTG GTG GAG			1347
167	Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu			
168	330	335	340	
169				
170	AAC GTG CCC CCG TTG CGC TGG AAG GAA TTC GTG CGG CGC CTA GGG CTG			1395
171	Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu			
172	345	350	355	
173				
174	AGC GAC CAC GAG ATC GAT CGG CTG GAG CTG CAG AAC GGG CGC TGC CTG			1443
175	Ser Asp His Glu Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu			
176	360	365	370	375
177				
178	CGC GAG GCG CAA TAC AGC ATG CTG GCG ACC TGG AGG CGG CGC ACG CCG			1491
179	Arg Glu Ala Gln Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro			
180	380	385	390	
181				
182	CGG CGC GAG GCC ACG CTG GAG CTG CTG GGA CGC GTG CTC CGC GAC ATG			1539
183	Arg Arg Glu Ala Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met			
184	395	400	405	
185				
186	GAC CTG CTG GGC TGC CTG GAG GAC ATC GAG GAG GCG CTT TGC GGC CCC			1587
187	Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro			
188	410	415	420	
189				
190	GCC GCC CTC CCG CCC GCG CCC AGT CTT CTC AGA TGAGGCTGCG CCCTGCGGGC			1640
191	Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg			
192	425	430		
193				
194	AGCTCTAAGG ACCGTCCTGC GAGATCGCCT TCCAACCCCA CTTTTTCTG GAAAGGAGGG			1700
195				
196	GTCCTGCAGG GGCAAGCAGG AGCTAGCAGC CGCCTACTTG GTGCTAACCC CTCGATGTAC			1760
197				
198	ATAGCTTTTC TCAGCTGCCT GCGCGCCGCC GACAGTCAGC GCTGTGCGCG CGGAGAGAGG			1820
199				
200	TGCGCCGTGG GCTCAAGAGC CTGAGTGGGT GGTGTGCGAG GATGAGGGAC GCTATGCCTC			1880
201				
202	ATGCCCCGTTT TGGGTGTCCT CACCAGCAAG GCTGCTCGGG GGCCCCCTGGT TCGTCCCTGA			1940
203				
204	GCCTTTTTCA CAGTGCATAA GCAGTTTTTTT TTGTTTTTGT TTTGTTTTGT TTTGTTTTTA			2000
205				
206	AATCAATCAT GTTACACTAA TAGAACTTG GCACTCCTGT GCCCTCTGCC TGGACAAGCA			2060
207				
208	CATAGCAAGC TGAAGTGTCC TAAGGCAGGG GCGAGCACGG AACAAATGGGG CCTTCAGCTG			2120
209				
210	GAGCTGTGGA CTTTTGTACA TACACTAAAA TTCTGAAGTT AAAAAAAAAA AAAAA			2175
211				
212				

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213 (2) INFORMATION FOR SEQ ID NO:2:

214

215 (i) SEQUENCE CHARACTERISTICS:

216 (A) LENGTH: 455 amino acids

217 (B) TYPE: amino acid

218 (D) TOPOLOGY: linear

219

220 (ii) MOLECULE TYPE: protein

221

222 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

223

224 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu

225 -21 -20 -15 -10

226

227 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro

228 -5 1 5 10

229

230 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys

231 15 20 25

232

233 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys

234 30 35 40

235

236 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp

237 45 50 55

238

239 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu

240 60 65 70 75

241

242 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val

243 80 85 90

244

245 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg

246 95 100 105

247

248 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe

249 110 115 120

250

251 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu

252 125 130 135

253

254 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu

255 140 145 150 155

256

257 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr

258 160 165 170

259

260 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser

261 175 180 185

262

263 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu

264 190 195 200

265

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266 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
267 205 210 215
268
269 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
270 220 225 230 235
271
272 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
273 240 245 250
274
275 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
276 255 260 265
277
278 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
279 270 275 280
280
281 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
282 285 290 295
283
284 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
285 300 305 310 315
286
287 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
288 320 325 330
289
290 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
291 335 340 345
292
293 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
294 350 355 360
295
296 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
297 365 370 375
298
299 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
300 380 385 390 395
301
302 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
303 400 405 410
304
305 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
306 415 420 425
307
308 Pro Ala Pro Ser Leu Leu Arg
309 430
310
311 (2) INFORMATION FOR SEQ ID NO:3:
312
313 (i) SEQUENCE CHARACTERISTICS:
314 (A) LENGTH: 26 base pairs
315 (B) TYPE: nucleic acid
316 (C) STRANDEDNESS: single
317 (D) TOPOLOGY: linear
318

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319 (ii) MOLECULE TYPE: protein
320
321
322
323 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
324
325 GGNGTYCCNT TYATRTARGT DGGNGT 26
326
327 (2) INFORMATION FOR SEQ ID NO:4:
328
329 (i) SEQUENCE CHARACTERISTICS:
330 (A) LENGTH: 17 base pairs
331 (B) TYPE: nucleic acid
332 (C) STRANDEDNESS: single
333 (D) TOPOLOGY: linear
334
335 (ii) MOLECULE TYPE: cDNA
336
337
338
339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
340
341 GGNGTYCCNT TYATRTA 17
342
343 (2) INFORMATION FOR SEQ ID NO:5:
344
345 (i) SEQUENCE CHARACTERISTICS:
346 (A) LENGTH: 17 base pairs
347 (B) TYPE: nucleic acid
348 (C) STRANDEDNESS: single
349 (D) TOPOLOGY: linear
350
351 (ii) MOLECULE TYPE: cDNA
352
353 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
354
355 TTYATRTARG TDGGNGT 17
356
357 (2) INFORMATION FOR SEQ ID NO:6:
358
359 (i) SEQUENCE CHARACTERISTICS:
360 (A) LENGTH: 27 base pairs
361 (B) TYPE: nucleic acid
362 (C) STRANDEDNESS: single
363 (D) TOPOLOGY: linear
364
365 (ii) MOLECULE TYPE: cDNA
366
367
368
369 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
370
371 CGGCCGATGG GCCTCTCCAC CGTGCCT 27

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372

373 (2) INFORMATION FOR SEQ ID NO:7:

374

375 (i) SEQUENCE CHARACTERISTICS:

376 (A) LENGTH: 27 base pairs

377 (B) TYPE: nucleic acid

378 (C) STRANDEDNESS: single

379 (D) TOPOLOGY: linear

380

381 (ii) MOLECULE TYPE: cDNA

382

383

384

385 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

386

387 AATAGTATTT CTAATCTGGG GTAGGCA

27

388

389 (2) INFORMATION FOR SEQ ID NO:8:

390

391 (i) SEQUENCE CHARACTERISTICS:

392 (A) LENGTH: 6 amino acids

393 (B) TYPE: amino acid

394 (C) STRANDEDNESS: single

395 (D) TOPOLOGY: linear

396

397 (ii) MOLECULE TYPE: peptide

398

399 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

400

401 Met Asp Ser Val Cys Pro

402 1 5

403

404 (2) INFORMATION FOR SEQ ID NO:9:

405

406 (i) SEQUENCE CHARACTERISTICS:

407 (A) LENGTH: 23 base pairs

408 (B) TYPE: nucleic acid

409 (C) STRANDEDNESS: single

410 (D) TOPOLOGY: linear

411

412 (ii) MOLECULE TYPE: cDNA

413

414

415

416 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

417

418 AATTCATGGA TAGTGTGTGT CCC

23

419

420 (2) INFORMATION FOR SEQ ID NO:10:

421

422 (i) SEQUENCE CHARACTERISTICS:

423 (A) LENGTH: 23 base pairs

424 (B) TYPE: nucleic acid

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425 (C) STRANDEDNESS: single

426 (D) TOPOLOGY: linear

427

428 (ii) MOLECULE TYPE: cDNA

429

430

431

432 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

433

434 GTACCTATCA CACACAGGGG TTC

23

435

436 (2) INFORMATION FOR SEQ ID NO:11:

437

438 (i) SEQUENCE CHARACTERISTICS:

439 (A) LENGTH: 22 amino acids

440 (B) TYPE: amino acid

441 (C) STRANDEDNESS: single

442 (D) TOPOLOGY: linear

443

444 (ii) MOLECULE TYPE: peptide

445

446

447 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

448

449 Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys

450 1 5 10 15

451

452 Arg Leu Arg Glu Tyr Tyr

453 20

454

455 (2) INFORMATION FOR SEQ ID NO:12:

456

457 (i) SEQUENCE CHARACTERISTICS:

458 (A) LENGTH: 7 amino acids

459 (B) TYPE: amino acid

460 (C) STRANDEDNESS: single

461 (D) TOPOLOGY: linear

462

463 (ii) MOLECULE TYPE: cDNA

464

465

466

467 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

468

469 Leu Cys Ala Pro Leu Arg Lys

470 1 5

471

472 (2) INFORMATION FOR SEQ ID NO:13:

473

474 (i) SEQUENCE CHARACTERISTICS:

475 (A) LENGTH: 9 amino acids

476 (B) TYPE: amino acid

477 (C) STRANDEDNESS: single

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478 (D) TOPOLOGY: linear
479
480 (ii) MOLECULE TYPE: peptide
481
482
483
484 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
485
486 Cys Arg Pro Gly Phe Gly Val Ala Arg
487 1 5
488
489 (2) INFORMATION FOR SEQ ID NO:14:
490
491 (i) SEQUENCE CHARACTERISTICS:
492 (A) LENGTH: 11 amino acids
493 (B) TYPE: amino acid
494 (C) STRANDEDNESS: single
495 (D) TOPOLOGY: linear
496
497 (ii) MOLECULE TYPE: peptide
498
499
500 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
501
502 Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
503 1 5 10
504
505 (2) INFORMATION FOR SEQ ID NO:15:
506
507 (i) SEQUENCE CHARACTERISTICS:
508 (A) LENGTH: 12 amino acids
509 (B) TYPE: amino acid
510 (C) STRANDEDNESS: single
511 (D) TOPOLOGY: linear
512
513 (ii) MOLECULE TYPE: peptide
514
515
516
517 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
518
519 Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser
520 1 5 10
521
522 (2) INFORMATION FOR SEQ ID NO:16:
523
524 (i) SEQUENCE CHARACTERISTICS:
525 (A) LENGTH: 8 amino acids
526 (B) TYPE: amino acid
527 (C) STRANDEDNESS: single
528 (D) TOPOLOGY: linear
529
530 (ii) MOLECULE TYPE: peptide

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531
532
533
534 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
535
536 Ser Cys Gly Pro Ser Tyr Pro Asp
537 1 5
538
539 (2) INFORMATION FOR SEQ ID NO:17:
540
541 (i) SEQUENCE CHARACTERISTICS:
542 (A) LENGTH: 13 amino acids
543 (B) TYPE: amino acid
544 (C) STRANDEDNESS: single
545 (D) TOPOLOGY: linear
546
547 (ii) MOLECULE TYPE: peptide
548
549
550 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
551
552 Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg
553 1 5 10
554
555 (2) INFORMATION FOR SEQ ID NO:18:
556
557 (i) SEQUENCE CHARACTERISTICS:
558 (A) LENGTH: 13 amino acids
559 (B) TYPE: amino acid
560 (C) STRANDEDNESS: single
561 (D) TOPOLOGY: linear
562
563 (ii) MOLECULE TYPE: peptide
564
565
566
567 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
568
569 Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
570 1 5 10
571
572 (2) INFORMATION FOR SEQ ID NO:19:
573
574 (i) SEQUENCE CHARACTERISTICS:
575 (A) LENGTH: 9 amino acids
576 (B) TYPE: amino acid
577 (C) STRANDEDNESS: single
578 (D) TOPOLOGY: linear
579
580 (ii) MOLECULE TYPE: peptide
581
582
583

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584 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

585

586 Pro Gly Trp Tyr Cys Ala Leu Ser Lys

587 1 5

588

589 (2) INFORMATION FOR SEQ ID NO:20:

590

591 (i) SEQUENCE CHARACTERISTICS:

592 (A) LENGTH: 17 amino acids

593 (B) TYPE: amino acid

594 (C) STRANDEDNESS: single

595 (D) TOPOLOGY: linear

596

597 (ii) MOLECULE TYPE: peptide

598

599

600 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

601

602 Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys

603 1 5 10 15

604

605 Arg

606

607

608 (2) INFORMATION FOR SEQ ID NO:21:

609

610 (i) SEQUENCE CHARACTERISTICS:

611 (A) LENGTH: 15 amino acids

612 (B) TYPE: amino acid

613 (C) STRANDEDNESS: single

614 (D) TOPOLOGY: linear

615

616 (ii) MOLECULE TYPE: peptide

617

618

619

620 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

621

622 Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg

623 1 5 10 15

624

625 (2) INFORMATION FOR SEQ ID NO:22:

626

627 (i) SEQUENCE CHARACTERISTICS:

628 (A) LENGTH: 9 amino acids

629 (B) TYPE: amino acid

630 (C) STRANDEDNESS: single

631 (D) TOPOLOGY: linear

632

633 (ii) MOLECULE TYPE: peptide

634

635

636

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637 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

638

639 Cys Arg Pro Gly Phe Gly Val Ala Arg

640 1 5

641

642 (2) INFORMATION FOR SEQ ID NO:23:

643

644 (i) SEQUENCE CHARACTERISTICS:

645 (A) LENGTH: 13 amino acids

646 (B) TYPE: amino acid

647 (C) STRANDEDNESS: single

648 (D) TOPOLOGY: linear

649

650 (ii) MOLECULE TYPE: peptide

651

652

653

654 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

655

656 Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser

657 1 5 10

658

659 (2) INFORMATION FOR SEQ ID NO:24:

660

661 (i) SEQUENCE CHARACTERISTICS:

662 (A) LENGTH: 20 amino acids

663 (B) TYPE: amino acid

664 (C) STRANDEDNESS: single

665 (D) TOPOLOGY: linear

666

667 (ii) MOLECULE TYPE: peptide

668

669

670

671 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

672

673 Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly

674 1 5 10 15

675

676 Thr Phe Ser Lys

677 20

678

679 (2) INFORMATION FOR SEQ ID NO:25:

680

681 (i) SEQUENCE CHARACTERISTICS:

682 (A) LENGTH: 20 amino acids

683 (B) TYPE: amino acid

684 (C) STRANDEDNESS: single

685 (D) TOPOLOGY: linear

686

687 (ii) MOLECULE TYPE: peptide

688

689

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690 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

691

692 Cys Arg Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp

693 1 5 10 15

694

695 Val Val Cys Lys

696 20

697

698 (2) INFORMATION FOR SEQ ID NO:26:

699

700 (i) SEQUENCE CHARACTERISTICS:

701 (A) LENGTH: 18 amino acids

702 (B) TYPE: amino acid

703 (C) STRANDEDNESS: single

704 (D) TOPOLOGY: linear

705

706 (ii) MOLECULE TYPE: peptide

707

708

709

710 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

711

712 Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln

713 1 5 10 15

714

715 Leu Trp

716

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/625,668A

DATE: 05/08/92
TIME: 06:31:53

LINE ERROR

ORIGINAL TEXT

33 Wrong application Serial Number

(A) APPLICATION NUMBER: US 07/625668

10

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SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/625,668A

DATE: 05/08/92
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MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

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SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/07/625,668A

DATE: 05/08/92
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CORRECTED TEXT